

IN THE SPECIFICATION:

At page 5, line 19, please amend the specification to correct the sequence as follows:

--variable region of the light chain (V_L). While the complementarity determining regions (CDRs) of the polypeptides amino acid sequence comprises a amino acid sequences that are substantially identical to amino acid sequence Ser-Tyr-Ala-Met-His (CDR1), Val-Ile-Ser-Tyr-Asp-Gly-Ser-Asn-Lys-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly (CDR2) and Asp-Arg-Leu-Ala-Val-Ala-Gly-Lys-Thr-Arg-Pro-Phe-Asp-Tyr (CDR3) of SEQ ID No 3 of the variable region of the heavy chain (V_H).--

Please amend page 27, lines 17-21, to correct the obvious error from grams to milligrams as follows:

--Figure 10a and 10b show the results of the *in-vivo* experiments with tumor-inoculated mice which were treated with SAM-6 antibody or a control antibody. According to Figure 10a the average weight of tumors of SAM-6 treated mice is 96.2 gram milligrams, while average weight of tumors of mice treated with control antibody is 150.5 gram milligrams.--

At page 61, line 24, please amend the specification to insert the biological deposit information for SAM-6 monoclonal producing hybridoma as follows:

--As described above, we obtained the SAM-6 monoclonal antibody expressing hybridoma (DSM ACC2903, deposited April 17, 2008, DSMZ, Inhoffenstr. 7B D-38124 Braunschweig) by fusing lymphocytes obtained from the spleen or lymph nodes of a cancer patient with the heteromyeloma cell line HAB-1 (faller, et al., Br. J. Cancer 62:595-598, 1990). The lymphoid sources were not pre-selected in terms of the age or sex of--

At page 62, line 29, please amend the specification to correct the sequence as follows:

--complementarity-determining regions (CDRs) of the polypeptides amino acid sequence comprises a amino acid sequences that are substantially identical to amino acid sequence Ser-Tyr-Ala-Met-His (CDR1), Val-Ile-Ser-Tyr-Asp-Gly-Ser-Asn-Lys-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly (CDR2) and Asp-Arg-Leu-Ala-Val-Ala-Gly-Lys-Thr-Arg-Pro-Phe-Asp-Tyr (CDR3) of SEQ ID No 3 of the variable region of the heavy chain (V_H).--